

10/554387 SEQ ID NO:8

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RESULT 11
US-10-554-387-14
; Sequence 14, Application US/10554387
; Publication No. US20060204487A1
; GENERAL INFORMATION:
; APPLICANT: Shauliel, Yoseph
; APPLICANT: Baum, Gideon
; APPLICANT: Sharon Hashmueli
; APPLICANT: Ayala Lewkowicz
; APPLICANT: Bartfeld, Daniel
; TITLE OF INVENTION: PRODUCTION OF HIGH MANNOSE PROTEINS IN PLANT CULTURE
; FILE REFERENCE: 30570
; CURRENT APPLICATION NUMBER: US/10/554,387
; CURRENT FILING DATE: 2005-10-25
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 14
; LENGTH: 526
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: High mannose human glucocerebrosidase (GCD)
US-10-554-387-14

Query Match          99.3%; Score 2648.5; DB 5; Length 526;
Best Local Similarity 99.6%; Pred. No. 1.1e-253;
Matches 495; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy      1 ARPCIPKSFYSSVVCVNATYCDSDPPTFPALGTFSTRYESTRSGRRMELSMGPIQANH 60
Db      23 ARPCIPKSFYSSVVCVNATYCDSDPPTFPALGTFSTRYESTRSGRRMELSMGPIQANH 82

Qy      61 TGTGLLLTLQPEQKFKVKVGGAMTDAALNLTALSPPAQNLLKSYFSEEGICYNIIIR 120
Db      83 TGTGLLLTLQPEQKFKVKVGGAMTDAALNLTALSPPAQNLLKSYFSEEGICYNIIIR 142

Qy      121 VPMASCDFSIRTYTYADTPDDFQLHNFSLPEEDTKLKIPLIHRALQLAQRVSLLASPWT 180
Db      143 VPMASCDFSIRTYTYADTPDDFQLHNFSLPEEDTKLKIPLIHRALQLAQRVSLLASPWT 202

Qy      181 SPTMLKTNGAVNGKSLKGQPGDIYHQTWARYFVKFLDAYAEHKLQFMAVTAENEPSAGL 240
Db      203 SPTMLKTNGAVNGKSLKGQPGDIYHQTWARYFVKFLDAYAEHKLQFMAVTAENEPSAGL 262

Qy      241 LSGYPFQCLGFTPEHQRFDIARDLGPTLANSTHHNVRLMLDDGRLLL-THAKVVLTDPE 299
Db      263 LSGYPFQCLGFTPEHQRFDIARDLGPTLANSTHHNVRLMLDDGRLLLPHWAKVVLTDPE 322

Qy      300 AAKYVHGIAVHWYLDLAPAKATLGETHRLFPNTMLFASEACVGSKFWEQSVRLGSDWGR 359
Db      323 AAKYVHGIAVHWYLDLAPAKATLGETHRLFPNTMLFASEACVGSKFWEQSVRLGSDWGR 382

Qy      360 MQYSHSIITNLLYHVVGWTDWNLALNPEGGPNWVRNFVDSPIIIVDITKDTFYKQPMFYHL 419
Db      383 MQYSHSIITNLLYHVVGWTDWNLALNPEGGPNWVRNFVDSPIIIVDITKDTFYKQPMFYHL 442

Qy      420 GHFSKFIPEGSRVGLVASQKNDLDAVALMHPDGSVAVVVVLRSSKDVPLTIKDPVAVGFL 479
Db      443 GHFSKFIPEGSRVGLVASQKNDLDAVALMHPDGSVAVVVVLRSSKDVPLTIKDPVAVGFL 502

Qy      480 ETISPGYSIHTYLMHRQ 496
Db      503 ETISPGYSIHTYLMHRQ 519

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SEQ ID NO:7

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RESULT 11
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; APPLICANT: Shaaltiel, Yoseph
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; LENGTH: 526
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: High mannose human glucocerebrosidase (GCD)
US-10-554-387-14
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Alignment Scores:

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Pred. No.: 1,48e-203 Length: 526
Score: 2673.00 Matches: 497
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 96.8% Indels: 0
DB: 5 Gaps: 0
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US-10-554-387A-7 (1-1491) x US-10-554-387-14 (1-526)

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Qy 1 GCCCGCCCCCTGCATCCCTAAAAGCTTCGGCTACAGCTCGGTGGTGTGTCTGCAATGCC 60
Db 23 AlaArgProCysIleProLysSerPheGlyTyrSerSerValValCysValCysAla 42

Qy 61 ACATACTGTGACTCCITTGACCCCCGACCTTTCTGCGCTTGGTACCTTCAGCCGCTAT 120
Db 43 ThrTyrCysAspSerPheAspProProThrPheProAlaLeuGlyThrPheSerArgTyr 62

Qy 121 GAGAGTACACGCGAGTGGGCGACGGATGGAGCTGAGTATGGGGCCATCCAGGCTAATCAC 180
Db 63 GluSerThrArgSerGlyArgArgMetGluLeuSerMetGlyProIleGlnAlaAsnHis 82

Qy 181 ACGGGCACAGGCGCTGCTACTGACCCCTGCAGCCAGAACAGAGTTCCAGAAAGTGAAGGA 240
Db 83 ThrGlyThrGlyLeuLeuLeuLeuGlnProGluGlnLysPheGlnLysValLysGly 102

Qy 241 TTGGAGGGGGCCATGACAGATGCTGCTGCTCTCAACATCCTTGCCCTGTCAACCCCTGCC 300
Db 103 PheGlyGlyAlaMetThrAspAlaAlaAlaLeuAsnIleLeuAlaLeuSerProProAla 122

Qy 301 CAAAATTGTACTTAAATCGTACTTCTCTGAAGAAGGAATCGGATATAACATCATCCGG 360
Db 123 GlnAsnLeuLeuLeuLysSerTyrPheSerGluGlyIleGlyTyrAsnIleIleArg 142

Qy 361 GTACCCATGGCCAGCTGTGACTTCTCCATCCGACCTACACCTATGCAGACACCCCTGAT 420
Db 143 ValProMetAlaSerCysAspPheSerIleArgThrTyrThrTyrAlaAspThrProAsp 162

Qy 421 GATTTCAGTTTGCACAACTTCAGCCTCCAGAGGAAGATACCAAGCTCAAGATACCCCTG 480
Db 163 AspPheGlnLeuHisAsnPheSerLeuProGluGluAspThrLysLeuLysIleProLeu 182

Qy 541 ATTCAACCGAGCCCTGCGAGTTGGCCCGCGTCCCGTTTCACTCCTTGCCAGCCCTGGACA 540
Db 183 IleHisArgAlaLeuGlnLeuAlaGlnArgProValSerLeuLeuAlaSerProThrThr 202

Qy 541 TCACCCACTTGGCTCAAGACCAATGGAGCGGTGAATGGGAAGGGGTCACTCAAGGGACAG 600
Db 203 SerProThrTrpLeuLysThrAsnGlyAlaValAsnGlyLysGlySerLeuLysGlyGln 222

Qy 601 CCCGGAGACATCTACCACCGACCTGGGCGAGATACCTTTGTGAAGTTCCGTATGCCTAT 660
Db 223
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Db 223 ProGlyAspIleTyrHisGlnThrTrpAlaArgTyrPheValLysPheLeuAspAlaTyr 242
 Qy 661 GCTGAGCACAGTTACAGTTCTGGGCGAGTACAGCTGAAAATGAGCCTTCTGCTGGCGTG 720
 Db 243 AlaGluHisLysLeuGlnPheTrpAlaValThrAlaGluAsnGluProSerAlaGlyLeu 262
 Qy 721 TTGATGGATACCCCTTCCAGTGGCTGGGCTTCACCCCTGAACATCAGCGAGACTTCATT 780
 Db 263 LeuSerGlyTyrProPheGlnCysLeuGlyPheThrProGluHisGlnArgAspPheIle 282
 Qy 781 GCGCTGACCTAGGTCCTACCCCTCGCCAAAGTACTACCCACAATGTCGGCTACTCATG 840
 Db 283 AlaArgAspLeuGlyProThrLeuAlaAsnSerThrHisHisAsnValArgLeuLeuMet 302
 Qy 841 CTGGATGACCAACGCTTCTGCTGCTGCCCAAGCTGGTACTGACAGACCCAGAA 900
 Db 303 LeuAspAspGlnArgLeuLeuLeuProHisTrpAlaLysValValLeuThrAspProGlu 322
 Qy 901 GCAGCTAAATATGTTTCATGGCATTGCTGTACATTGGTACCTGGACTTTCTGGCTCCAGCC 960
 Db 323 AlaAlaLysTyrValHisGlyIleAlaValHisTrpTyrLeuAspPheLeuAlaProAla 342
 Qy 961 AAAGCCACCTAGGGGAGACACACCCCTGTTCGCCAACCATGCTCTTTGCCTCAGAG 1020
 Db 343 LysAlaThrLeuGlyGluThrHisArgLeuPheProAsnThrMetLeuPheAlaSerGlu 362
 Qy 1021 GCGTGTGGGCTCCAAGTTCTGGGAGCAGAGTGTGGGCTAGGCTCCTGGGATCGAGGG 1080
 Db 363 AlaCysValGlySerLysPheTrpGluGlnSerValArgLeuGlySerTrpAspArgGly 382
 Qy 1081 ATGCAGTACAGCCACAGCATCATCACGAACCTCCTGTACCATGTGGTGGGTGGAACGAG 1140
 Db 383 MetGlnTyrSerHisSerIleIleThrAsnLeuLeuTyrHisValValGlyTrpThrAsp 402
 Qy 1141 TGGAAACCTTGGCCTGAACCCGAAGGAGGAGCCCAATTGGGTGCGTAACTTTGTGCGAGT 1200
 Db 403 TrpAsnLeuAlaLeuAsnProGluGlyGlyProAsnTrpValArgAsnPheValAspSer 422
 Qy 1201 CCCATCTTGTAGACATCACCAAGGACACGTTTTACAACAGCCCATGTTCTACCCACTT 1260
 Db 423 ProIleIleValAspIleThrLysAspThrPheTyrLysGlnProMetPheTyrHisLeu 442
 Qy 1261 GCGCACTTCAGCAAGTTCATTCTGAGGGCTCCAGAGAGTGGGGCTGGTGGCAGTCAG 1320
 Db 443 GlyHisPheSerLysPheIleProGluGlySerGlnArgValGlyLeuValAlaSerGln 462
 Qy 1321 AAGAACGACCTGGACGCGAGTGGCATGATGCATCCCGATGGCTCTGCTGTTGTGGTCTGT 1380
 Db 463 LysAsnAspLeuAspAlaValAlaLeuMetHisProAspGlySerAlaValValVal 482
 Qy 1381 CTAACCGCTCCTCTAAGGATGTGCTCTTACCATCAAGGATCCTGCTGTGGGCTTCCTG 1440
 Db 483 LeuAsnArgSerSerLysAspValProLeuThrIleLysAspProAlaValGlyPheLeu 502
 Qy 1441 GAGACAACTCTACCTGGCTACTCCATTACACACTACCTGTGGCATCGCCAG 1491
 Db 503 GluThrIleSerProGlyTyrSerIleHisThrTyrLeuTrpHisArgGln 519